**REMARKS**

Applicants have added into the present specification a new paper copy Sequence Listing section according to 37 C.F.R. §1.821(c) as new pages 1-6. Furthermore, attached hereto is a 3 1/2" disk containing the "Sequence Listing" in computer readable form in accordance with 37 C.F.R. §1.821(e).

Applicants have amended the specification to insert SEQ ID Nos, as supported in the present specification.

The following statement is provided to meet the requirements of 37 C.F.R. §1.821(f) and 1.821(g).

I hereby state, in accordance with 37 C.F.R. §1.821(f), that the content of the attached paper and computer readable copies of the sequence listing are believed to be the same.

I hereby also state, in accordance with 37 C.F.R. §1.821(g), that the submission is not believed to include new matter.

Under U.S. rules, each sequence must be classified in <213> as an "Artificial Sequence", a sequence of "Unknown" origin, or a sequence originating in a particular organism, identified by its scientific name.

Neither the rules nor the MPEP clarify the nature of the relationship which must exist between a listed sequence and an organism for that organism to be identified as the origin of the sequence under <213>.

Hence, counsel may choose to identify a listed sequence as associated with a particular organism even though

that sequence does not occur in nature by itself in that organism (it may be, e.g., an epitopic fragment of a naturally occurring protein, or a cDNA of a naturally occurring mRNA, or even a substitution mutant of a naturally occurring sequence). Hence, the identification of an organism in <213> should not be construed as an admission that the sequence *per se* occurs in nature in said organism.

Similarly, designation of a sequence as "artificial" should not be construed as a representation that the sequence has no association with any organism. For example, a primer or probe may be designated as "artificial" even though it is necessarily complementary to some target sequence, which may occur in nature. Or an "artificial" sequence may be a substitution mutant of a natural sequence, or a chimera of two or more natural sequences, or a cDNA (i.e., intron-free sequence) corresponding to an intron-containing gene, or otherwise a fragment of a natural sequence.

The Examiner should be able to judge the relationship of the enumerated sequences to natural sequences by giving full consideration to the specification, the art cited therein, any further art cited in an IDS, and the results of his or her sequence search against a database containing known natural sequences.

Attached hereto is a marked-up version of the changes made to the specification and claims by the current amendment. The attached page is captioned "Version with markings to show changes made".

Applicants submit that the present application contains patentable subject matter and therefore urge the examiner to pass the case to issuance.

If the examiner has any questions or comments concerning the above described application, the examiner is urged to contact the undersigned at the phone number below.

Respectfully submitted,

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the specification:

The paragraph beginning at line 5 of page 5 has been amended as follows:

(i) a peptide of at least 4 amino acid residues comprising a sequence selected from:

(a) Thr - Pro - Arg - Val (residues 1-4 of SEQ ID NO:1)

(b) Lys - Ala - Thr - Phe (residues 3-6 of SEQ ID NO:4)

(c) Leu - Arg - Val - Tyr (residues 4-7 of SEQ ID NO:7)

The three paragraphs beginning at line 21 of page 5 and ending at line 5 of page 6 have been amended as follows:

In one embodiment, a peptide according to (i)(a) above has a sequence selected from:

**(a1)** Leu Lys Thr Pro Arg Val (SEQ ID NO:1)

**(a2)** Lys Thr Pro Arg Val Thr (SEQ ID NO:2)

**(A)** Asn Thr Leu Lys Thr Pro Arg Val Gly Gly (SEQ ID NO:3)

In another embodiment, a peptide according to (i)(b) above has a sequence selected from:

**(b1)** Lys Asp Lys Ala Thr Phe (residues 1-6 of SEQ ID NO:4)

**(B)** Lys Asp Lys Ala Thr Phe Gly Thr His Asp Gly (SEQ ID NO:4)

In a further embodiment, a peptide according to (i)(c) above has a sequence selected from:

**(c1)** Thr Leu Arg Val Tyr Lys (residues 3-8 of SEQ ID

NO:7)

**(c2)** Thr Lys Leu Arg Val Tyr (SEQ ID NO:5)

**(c3)** Thr Leu Leu Arg Val Tyr (SEQ ID NO:6)

**(C)** Cys Ala Thr Leu Arg Val Tyr Lys Gly Gly (SEQ ID NO:7)

The paragraph beginning at line 4 of page 13 has been amended as follows:

Examples of divalent peptides with peptides derived from monopeptides **A-C** of the invention and irrelevant peptide **D** are as follows:

**A:** Asn Thr Leu Lys Thr Pro Arg Val Gly Gly X Ala (SEQ ID NO:8)

**B:** Lys Asp Lys Ala Thr Phe Gly Thr His Asp Gly Gly X Ala (SEQ ID NO:9)

**C:** Cys Ala Thr Leu Arg Val Tyr Lys Gly Gly Gly X Ala (SEQ ID NO:10)

**D:** Pro Val Arg Ser Pro His Gln Ser Tyr Pro Gly Gly Gly X Ala (SEQ ID NO:11)

wherein X=FmocLys(Fmoc)-OH

Table 1 on page 22 has been amended as follows:

**Table 1**

**Binding of anti-β2GPI mAbs to phage isolated from an hexapeptide epitope library**

| Antibody | Epitope sequence* | SEQ ID NO: | Binding O.D. | Phages identified, no. |
|---|---|---|---|---|
| ILA-1 | L **K T P R V** | 8 (res. 3-8) | 975 ± 72 | 24 |
| | **K T P R V** T | 12 | 1201 ± 142 | 18 |
| ILA-3 | K D **K A T F** | 13 | 1178 ± 101 | 15 |
| G-3 | T **L R V Y** K | 14 | 791 ± 33 | 12 |
| | T K **L R V Y** | 15 | 954 ± 62 | 7 |
| | T L **L R V Y** | 16 | 869 ± 71 | 16 |

The two paragraphs beginning at line 1 of page 23 and ending at line 11 of page 23 has been amended as follows:

ILA-1 mAb detected the sequence KTPRV (residues 4-8 of SEQ ID NO:8) that appeared in 42 clones, wherefrom 24 clones showed the sequence LKTPRV (residues 3-8 of SEQ ID NO:8) which represents a mimotope located between domain I/II of the β2GPI molecule as LK(C)TPRV (SEQ ID NO:17) on the native form of the β2GPI . The other 18 clones showed the motif KTPRVT (SEQ ID NO12) presented at the same location on the β2GPI and appearing as K(C)TPRV(CC)T (SEQ ID NO:18).

ILA-3 mAb fished out the linear sequence KDKATF (SEQ ID NO:13) located on the fourth domain of the β2GPI molecule (15 clones). ILA-4 mAb probed the sequence mimotope LVEPWR (SEQ ID NO:19) the location of which on β2GPI is still undetermined. The anti-β2GPI mAb named G-3 recognized a linear motif sequence LRVY (residues 3-6 of SEQ ID NO:15) located on

the third domain of the β2GPI molecule, that appeared in 37 of the examined clones.

**In the claims:**

Claims 2-5, 10, 14 and 15 have been amended as follows:

2 (Amended). The peptide or derivative according to claim 1, being selected from the group consisting of:

(i) a peptide of at least 4 amino acid residues comprising a sequence selected from:

(a) Thr Pro Arg Val (residues 1-4 of SEQ ID NO:1)

(b) Lys Ala Thr Phe (residues 3-6 of SEQ ID NO:4)

(c) Leu Arg Val Tyr (residues 4-7 of SEQ ID NO:7)

(ii) a cyclic derivative of a peptide of (i);

(iii) a peptide according to (i) or (ii) in which one or more amino acid residues have been replaced by the corresponding D-isomer or by a non-natural amino acid residue;

(iv) a chemical derivative of a peptide according to (i) - (iii);

(v) a multichain peptide-oligomer/polymer conjugate comprising two or more of the same or different peptides or peptide derivatives (i) to (iv) attached to a native or synthetic multifunctional oligomeric or polymeric backbone; and

(vi) a multiple antigen peptide in which two to eight same or different peptides or peptide derivatives (i) to (iv) are anchored onto a diaminoalkanoic acid core.

3 (Amended). The peptide according to claim 2 (i)(a) of a sequence selected from:

Leu Lys Thr Pro Arg Val (SEQ ID NO:1)

Lys Thr Pro Arg Val Thr (SEQ ID NO:2)

Asn Thr Leu Lys Thr Pro Arg Val Gly Gly (SEQ ID NO:3).

4 (Amended). The peptide according to claim 2 (i)(b) of a sequence selected from:

Lys Asp Lys Ala Thr Phe (residues 1-6 of SEQ ID NO:4)

Lys Asp Lys Ala Thr Phe Gly Thr His Asp Gly (SEQ ID NO:4).

5 (Amended). The peptide according to claim 2 (i)(c) of a sequence selected from:

Thr Leu Arg Val Tyr Lys (residues 3-8 of SEQ ID NO:7)

Thr Lys Leu Arg Val Tyr (SEQ ID NO:5)

Thr Leu Leu Arg Val Tyr (SEQ ID NO:6)

Cys Ala Thr Leu Arg Val Tyr Lys Gly Gly (SEQ ID NO:7)

10 (Amended). The multichain peptide-oligomer/polymer conjugate according to claim 9 wherein the protein is streptavidin and the biotinylated peptide is selected from:

Asn Thr Leu Lys Thr Pro Arg Val Gly Gly (residues 1-10 of SEQ ID NO:8)

Lys Asp Lys Ala Thr Phe Gly Thr His Asp Gly (residues 1-11 of SEQ ID NO:9)

Cys Ala Thr Leu Arg Val Tyr Lys Gly Gly (residues 1-10 of SEQ ID NO:10).

14 (Amended). The multiple antigen peptide according to claim 13 wherein the spacer is Ala and the diaminoalkanoic acid core is $Fmoc_2$-Lys-Ala onto which are anchored two peptides selected from:

Asn Thr Leu Lys Thr Pro Arg Val Gly Gly (residues 1-10 of SEQ ID NO:8)

Lys Asp Lys Ala Thr Phe Gly Thr His Asp Gly (residues 1-11 of SEQ ID NO:9)

Cys Ala Thr Leu Arg Val Tyr Lys Gly Gly (residues 1-10 of SEQ ID NO:10).

15 (Amended). The multiple antigen peptide according to claim 13 wherein the spacer is Ala and the diaminoalkanoic acid core is $Fmoc_4$-$Lys_2$-Ala onto which are anchored four peptides selected from:

Asn Thr Leu Lys Thr Pro Arg Val Gly Gly (residues 1-10 of SEQ ID NO:8)

Lys Asp Lys Ala Thr Phe Gly Thr His Asp Gly (residues 1-11 of SEQ ID NO:9)

Cys Ala Thr Leu Arg Val Tyr Lys Gly Gly (residues 1-10 of SEQ ID NO:10).